

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2002, 14:26:09 ; Search time 2530 Seconds
(without alignments)

Title: US-09-635-501-1
Perfect score: 3396
Sequence: 1 gaattcggttcctcctaa.....aaaaaaaaagggcgccgc 3396

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthu:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES | | | |
|------------|-------|-------------|-------------|
| Result No. | Score | Query Match | Description |
| 1 | 984.6 | 29.0 | AL551235 |
| 2 | 969.8 | 28.6 | AL574873 |
| 3 | 795.2 | 23.4 | AK008530 |
| 4 | 596.2 | 17.6 | BI913504 |
| 5 | 594.6 | 17.5 | BI561069 |
| 6 | 581.8 | 17.1 | BG722079 |
| 7 | 536.4 | 15.8 | BI561359 |
| 8 | 502.8 | 14.8 | BG962298 |
| 9 | 487.8 | 14.4 | BM460886 |
| 10 | 472.1 | 13.9 | BG401683 |
| 11 | 469.4 | 13.8 | BF789159 |
| 12 | 458.8 | 13.5 | AW772472 |
| 13 | 451.2 | 13.3 | BB52968 |
| 14 | 451.1 | 13.3 | BG428060 |
| 15 | 440.6 | 13.0 | AI628611 |
| 16 | 430.4 | 12.7 | AA397955 |
| 17 | 423.6 | 12.5 | AI831883 |

| | | | | | |
|------|-------|------|-----|----|----------|
| c 18 | 422.8 | 12.4 | 426 | 9 | AW271467 |
| c 19 | 421 | 12.4 | 434 | 9 | AA420969 |
| c 20 | 420.8 | 12.4 | 555 | 9 | AA162058 |
| 21 | 413.6 | 12.2 | 741 | 10 | BG772384 |
| 22 | 413.4 | 12.2 | 778 | 10 | BI831019 |
| 23 | 399 | 11.7 | 556 | 10 | BM030353 |
| 24 | 384.2 | 11.3 | 398 | 10 | BF091535 |
| c 25 | 384 | 11.3 | 386 | 9 | AA416585 |
| c 26 | 382.6 | 11.3 | 842 | 10 | BF784147 |
| c 27 | 356.6 | 10.5 | 422 | 9 | AW260204 |
| c 28 | 353 | 10.4 | 353 | 9 | AI928360 |
| c 29 | 349.4 | 10.3 | 351 | 9 | AW590883 |
| c 30 | 348 | 10.2 | 574 | 9 | AI116021 |
| c 31 | 344 | 10.1 | 347 | 9 | AW848579 |
| c 32 | 343.4 | 10.1 | 348 | 9 | AL039738 |
| c 33 | 342.4 | 10.1 | 471 | 9 | AW358360 |
| c 34 | 320.6 | 9.4 | 392 | 10 | BF334479 |
| c 35 | 318.8 | 9.4 | 459 | 9 | BE138336 |
| c 36 | 314.4 | 9.3 | 552 | 9 | AI036772 |
| c 37 | 312.6 | 9.2 | 432 | 9 | AW258861 |
| c 38 | 306 | 9.0 | 418 | 9 | BB687602 |
| c 39 | 301 | 8.9 | 301 | 9 | AA421125 |
| c 40 | 298 | 8.8 | 299 | 10 | BE843196 |
| c 41 | 284.2 | 8.4 | 501 | 10 | BM445902 |
| c 42 | 277.8 | 8.2 | 451 | 10 | BE722366 |
| c 43 | 257.2 | 7.6 | 312 | 9 | AW001638 |
| c 44 | 256.8 | 7.6 | 292 | 10 | BE843206 |
| c 45 | 247.8 | 7.3 | 426 | 9 | AI035384 |

ALIGNMENTS

RESULT 1
AL551235
LOCUS AL551235 LTI_NFL006.PL2 Homo sapiens cDNA clone CSODI041YM14 5 prime, mRNA sequence.
DEFINITION AL551235 LTI_NFL006.PL2 Homo sapiens cDNA clone CSODI041YM14 5 prime, mRNA sequence.
ACCESSION AL551235
VERSION AL551235.1 GI:12888986
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Li.W.B., Gruber.C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1. .987
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODI041YM14"
/clone_lib="LTI_NFL006.PL2"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
322 a 182 c 211 g 270 t
BASE COUNT 322 a 182 c 211 g 270 t 2 others
ORIGIN

987 bp mRNA linear EST 16-FEB-2001
Homo sapiens cDNA clone CSODI041YM14 5

| | | | | | |
|-----------------------|------|--|---------------------|-----------|-------------|
| Query Match | | 29.0%; | Score 984.6; | DB 9; | Length 987; |
| Best Local Similarity | | 99.7%; | Pred. No. 1.3e-193; | | |
| Matches 984; | | Conservative 2; | Mismatches 1; | Indels 0; | Gaps 0; |
| QY | 1661 | AAGCACTTTGTCAACGAGCTAAACATGAAGCCCTCTCCACAAATGTGACATCTCAAACT | 1720 | | |
| Db | 1 | AAGCACTTTGTCAACGAGCTAAACATGAAGCCCTCTCCACAAATGTGACATCTCAAACT | 60 | | |
| QY | 1721 | CTACAGAAGCTGGACAGAACTGTTCAATATGCTGAGGCTTGGAAATCAAGAACCCCTGGA | 1780 | | |
| Db | 61 | CTACAGAAGCTGGACAGAACTGTTCAATATGCTGAGGCTTGGAAATCAAGAACCCCTGGA | 120 | | |
| QY | 1781 | CCCTAGCATGGAATGTTGTAGAGCAAGAACATGAATGAAGGCCACTGCTCAACT | 1840 | | |
| Db | 121 | CCCTAGCATGGAATGTTGTAGAGCAAGAACATGAATGAAGGCCACTGCTCAACT | 180 | | |
| QY | 1841 | ACTTTGAGCCCTTATTACCTGGCTGAAAGACCAAGCAAGAAATCTTTTGGGATGGA | 1900 | | |
| Db | 181 | ACTTTGAGCCCTTATTACCTGGCTGAAAGACCAAGCAAGAAATCTTTTGGGATGGA | 240 | | |
| QY | 1901 | GTACCGACTGGAGTCCATATGCGACACCAAGCATCAAAAGTGAGGATAAGCCTAAATCAG | 1960 | | |
| Db | 241 | GTACCGACTGGAGTCCATATGCGACACCAAGCATCAAAAGTGAGGATAAGCCTAAATCAG | 300 | | |
| QY | 1961 | CTCTTGGAGATAAAGCATATGAATGGAACGACATGAATGTACTGTTCGATCATCTG | 2020 | | |
| Db | 301 | CTCTTGGAGATAAAGCATATGAATGGAACGACATGAATGTACTGTTCGATCATCTG | 360 | | |
| QY | 2021 | TTGCATATGCTATGAGGAGTACTTTTTAAAGTAAAAATCAGATGATCTTTTGGGG | 2080 | | |
| Db | 361 | TTGCATATGCTATGAGGAGTACTTTTTAAAGTAAAAATCAGATGATCTTTTGGGG | 420 | | |
| QY | 2081 | AGGAGATGTGGAGTGGCTAATTTGAACCAAGAAATCCCTTTAATTTCTTGTCACTG | 2140 | | |
| Db | 421 | AGGAGATGTGGAGTGGCTAATTTGAACCAAGAAATCCCTTTAATTTCTTGTCACTG | 480 | | |
| QY | 2141 | CACCTAAAAATGTGTCTCATATCTCTAGACTGAAGTTGAAAGGCCATCAGGATGT | 2200 | | |
| Db | 481 | CACCTAAAAATGTGTCTCATATCTCTAGACTGAAGTTGAAAGGCCATCAGGATGT | 540 | | |
| QY | 2201 | CCCGAGCGGTATCAATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGGGA | 2260 | | |
| Db | 541 | CCCGAGCGGTATCAATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGGGA | 600 | | |
| QY | 2261 | TACAGCCAACTTGGACCTCTTAACGAGCCCTCTTCCATATGGCTGATTTGTTTG | 2320 | | |
| Db | 601 | TACAGCCAACTTGGACCTCTTAACGAGCCCTCTTCCATATGGCTGATTTGTTTG | 660 | | |
| QY | 2321 | GAGTTGTGATGGAGTGATAGTGGTGGCATTTGTCATCTCTGATCTTCACTGGGATCAGAG | 2380 | | |
| Db | 661 | GAGTTGTGATGGAGTSATAGTGGTGGCATTTGTCATCTCTGATCTTCACTGGGATCAGAG | 720 | | |
| QY | 2381 | ATCGGAAGAAGAAATAAAGCAAGAGTGGAGAAATCCCTTATGCCCTCCATCATATTA | 2440 | | |
| Db | 721 | ATCGGAAGAAGAAATAAAGCAAGAGTGGAGAAATCCCTTATGCCCTCCATCATATTA | 780 | | |
| QY | 2441 | GCAAGGAGAAATAATCCAGATTCACAAACACTGATGTTTCCAGACCTCTTTTAGA | 2500 | | |
| Db | 781 | GCAAGGAGAAATAATCCAGATTCACAAACACTGATGTTTCCAGACCTCTCTTTAGA | 840 | | |
| QY | 2501 | AAAATCTATGTTTCTCTTCTGAGTGATTTGTTGTATGTAATGTTAATTTTCATGGTA | 2560 | | |
| Db | 841 | AAAATCTATGTTTCTCTTCTGAGTGATTTGTTGTATGTAATGTTAATTTTCATGGTA | 900 | | |
| QY | 2561 | TAGAAATATAGATGATAAGATATCAATTAATGTCAAAACATGACTCTGTTTCAGAAA | 2620 | | |
| Db | 901 | TAGAAATATAGATGATAAGATATCAATTAATGTCAAAACATGACTCTGTTTCAGAAA | 960 | | |
| QY | 2621 | AAAATTTCTCCAAAGACACATGCGCA | 2647 | | |
| Db | 961 | AAAATTTCTCCAAAGACACATGCGCA | 987 | | |

RESULT 2
AL574873/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

SOURCE

AL574873 1039 bp mRNA linear EST 16-FEB-2001
AL574873 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI041YM14 3
Prime, mRNA sequence.
AL574873
AL574873.1 GI:12935492
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1039)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

1. .1039
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 328 a 224 c 177 g 303 t 7 others

Query Match 28.6%; Score 969.8; DB 9; Length 1039;
Best Local Similarity 98.4%; Pred. No. 1.5e-190;
Matches 1026; Conservative 3; Mismatches 9; Indels 5; Gaps 5;

| | | | |
|----|------|---|------|
| QY | 2281 | CTTAACAGCCCTCTGTTCCATATGCTGATGCTTTGGAGTTGTGATGGAGTGATA | 2340 |
| Db | 1039 | CTTAACAGCCCTCTGTTCCATATGCTGATGCTTTGGAGTTGTGATGGAGTGATA | 982 |
| QY | 2341 | GTGGTTGGCATTGCTATCCTCTGATCTTCACTGGATCAGAGATCGGAAGAAATAAA | 2400 |
| Db | 981 | GTGGTTGGCATTGCTATCCTCTGATCTTCACTGGATCAGAGATCGGAAGAAATAAA | 922 |
| QY | 2401 | GCAAGAAGTGGAGAAATCCTTATGCTCCATCGATATTAGCAAGGAGAAATAATCCA | 2460 |
| Db | 921 | GCAAGAAGTGGAGAAATCCTTATGCTCCATCGATATTAGCAAGGAGAAATAATCCA | 862 |
| QY | 2461 | GGATTCGAAACACTGATGATGTTCCAGACCTCTTTTAGAAAAATCTATGTTTCTCT | 2520 |
| Db | 861 | GGATTCGAAACACTGATGATGTTCCAGACCTCTTTTAGAAAAATCTATGTTTCTCT | 802 |
| QY | 2521 | TGAGTGTGATTTCTCTGATGTAATCTTAATTTTCATGCTATAGAAATATAGATGATA | 2580 |
| Db | 801 | TGAGTGTGATTTCTCTGATGTAATCTTAATTTTCATGCTATAGAAATATAGATGATA | 742 |
| QY | 2581 | AGATATCAATAATGTCAAACTATGACTCTGTTCAG-AAAAAAAATGTCCAAAGACAA | 2639 |
| Db | 741 | AGATATCAATAATGTCAAACTATGACTCTGTTCAGAAATAAATAATGTCCAAAGACAA | 682 |
| QY | 2640 | CATGGCCAGGAGAGACATCTTCATTGACATGCTTTTTCAGTATTATTCTCTCTGG | 2699 |
| Db | 681 | CATGGCCAGGAGAGACATCTTCATTGACATGCTTTTTCAGTATTATTCTCTCTGG | 622 |
| QY | 2700 | ATTGACTTCTGTTCTGTTTCTTAAATAGGATTTTCTTATTAGAGTATATTAGGAAAGTG | 2759 |

ORIGIN

Query Match 23.4%; Score 795.2; DB 11; Length 1603;
Best Local Similarity 72.6%; Pred. No. 2.1e-154;
Matches 1203; Conservative 0; Mismatches 389; Indels 65; Gaps 11;
Qy 1702 AAATGTGACATCTCAAACTCTACAGAAGCTGGACAGAAATGTTCAATATGCTGAGGCTT 1761
Db 1 AANTGTGACATCTCAAAATCCAACTGGAAGCTGGGCGAAGTTGCTCAAGATGCTGAGTCTT 60
Qy 1762 GGAATAACAGAACCTCGACCTAGCATGGAAATCTGTAGGAGCAAAAGACATGAAT 1821
Db 61 GGAATTCAGAGCCCTGGACAAAGCCCTGGAAATGTGGTAGGAGCAAGAAATATGGAT 120
Qy 1822 GTAAGGCCACTGCTCAACTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAAGCAAG 1881
Db 121 CTAAACCACTGCTCAATTACTTCCAAACCGTTGTTGACTGGCTGNAAGAGCAAGACAGA 180
Qy 1882 AATTCCTTTTGGGATGGAGTACCGACTGGAGTCCATATGACAGACCAAAAGCAAAAGTG 1941
Db 181 AATTCCTTTTGGGATGGAGTACCGACTGGAATGGAGCCCATATGCCACCAAAAGCAATTAAGTG 240
Qy 1942 AGGATAAGCCATAAATCAGCTCTTGGAGATAAAGCATATGAATGGAACGACATGAATG 2001
Db 241 AGGATAAGCCATAAATCAGCTCTTGGAGCTAATGCATATGAATGGACCAACAGCAAGATG 300
Qy 2002 TACCTGTTCCGATCATCTGTTGCATATGCTATGAGGAGTACTTTTTTAAAGTAAAAAAT 2061
Db 301 TTCCTGTTCCGATCATCTGTTGCATATGCCATGAGAAGTATTTTCAATAATCAAAAAC 360
Qy 2062 CAGATGATCTTTTGGGAGGAGGATGTCGAGTGGCTAATTTGAAACCAAGATCTCC 2121
Db 361 CAGACAGTCTCTTTAGAGGAAGATGTACGAGTGAATTTGAAACCAAGAGTCTCC 420
Qy 2122 TTTAATCTTTTGTGCACTGCACTTAAATAATGTCATATCATCTCTAGAACTGGAAGTT 2181
Db 421 TTTACTTCTTTTGTGCACTGCACTTAAATAATGTCATATCATCTCTAGAACTGGAAGTT 480
Qy 2182 GAAAGGCCATCAGATGTCTCCGAGCCGATATCAATGATGCTTTCCGCTCTGAATGACAAC 2241
Db 481 GAAGATGCCATCAGATGTCTCCGAGCCGATATCAATGATGCTTTGCGCTGAATGATAAC 540
Qy 2242 AGCCTAGAGTTCTGGGATACACCAACACTTGGACCTCTTACACGCCCTCTGTTTCC 2301
Db 541 AGCCTAGAGTTCTGGGATACACCAACACTTGGACCACTTACACGCCCTCTGTTTCC 600
Qy 2302 ATATGGCTGATGTTTGTGGAGTTGTGATGGAGTGTAGTGGTGTGCTATGCTCCTG 2361
Db 601 ATATGGCTGATGTTTGTGGAGTTGTGATGGAGTGTAGTGGTGTGCTATGCTCCTG 660
Qy 2362 ATCTTCACTGGGATCAGAGATCGGAAGAAGAAAATAAAGCAAGAAGTGGAGAAAATCCT 2421
Db 661 ATTGCTACTGGGATCAAAAGTTCGAAGAAGAAAATAAAGCAAGAAGTGGAGAAAATCCT 720
Qy 2422 TATGCTCCATCGATATTTAGCAAGGAGAAATAATCCAGGATTCAAAACACTGATGAT 2481
Db 721 TATGACTCGATGAGCATTTGGAAGAGGAGAAAGCAATGCGAGGATTCAAAACACTGATGAT 780
Qy 2482 GTTCAGACTCTCTTTTAGAAAAATCTATGTTTTTCCCTCTTGAGTGTATTTGTTGATGT 2541
Db 781 GCTCAGACTCTCTTTTAGCAAGCACT-----TGTCATCTCTCTGATGT 824
Qy 2542 AAATGTTAATTCATGGTATGAAATATATAGATGATAAGATATCATTAATAGTCAAAA 2601
Db 825 AAATGCTAATTCATAGTACAAAAATATGAGATATACACATGCTATAGCTATCAAAA 884
Qy 2602 CTATGACTCTCTTCAGAAAAAAATTTGCCAAACACACATATGCGCCAGGAGAGACATCT 2661
Db 885 CTATGA---TCTGTGTAGTAAACGTTGTCCAAAG--AGCATCAGACTTGAAGTGACATCT 939
Qy 2662 TCATTGACATGCTTTTTCAGTATTTATTTCTCTCTGATTTGACTCTGTTCTGTTTCT 2721
Db 940 TCATGACATGCTTTTTCAGTATTTATTTCTGCTTAAGGATTTGACATCTCTCTGTTTAT 999

Qy 2722 TAATAAGGATTTTGTATTAGACTATATTAGGAAAGTGTGTATTTGGTCTCACAGGCTGT 2781
Db 1000 TAATACAGATGTTTATCTTAGCATAAAGAGGAAATGTGCCTTTGGCCTCACAGTCTAT 1059
Qy 2782 TCAGGAGTAATCTAAATGTAAATGCTGTGTGAATTTCTGAAGTTGAAAACAGGATATAT 2841
Db 1060 CCAGG-----TCATATGGTTGGTAACCTGGAGTTAGAAGATGAGATGATGCT 1108
Qy 2842 CATTTGAGCAAGTGTGGATCTTTGATGAATATGGATGGATCACTTTGAAGGACAGATGC 2901
Db 1109 CTTGGGGGCAAGTGTGGCTTCGGTGGGATCTG-----GG 1145
Qy 2902 CTGGGAGTGGTGTAGCTGCAAGGATTTGAGAATGGCATGCAATTAGCTCACTTTCAATTAA 2961
Db 1146 CTGTGAACCTGGTGGGACTGTTGAGGTTGAGAAATGGTCTCGCTGGTCACTTGAATCCAAAG 1205
Qy 2962 TCCATTTGTCAGG-ATGACATGCTTTCTTCACAGTAACCTCACTTCAAGTACTATGGTAT 3020
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Qy 3021 TTGCCTACAGTGTATGTTTGAATCGATCATGCTTTCTCAAGTGCACAGTCTAAAGAGA 3080
Db 1266 TTGTTACAGTAATACTTGAATGGAATGCTCCCTCTTTGGAGGTCCAGTTCAACGGAGA 1325
Qy 3081 GAAGAATCCAGGGAACAGGTAGAGGACATTTGCTTTTCACTTCCAAAGTGTGCTGATCAAC 3140
Db 1326 -AAGAAGCCAGACATCAGGTAGAGACATGAGCTTTCTCTTCCAAA---CTTGATCAAC 1381
Qy 3141 ATCTCCCTGACACACAAAACCTAGAGCCAGGGCCCTCCGTAACCTCCAGAGCATGCCCTG 3200
Db 1382 ATCTCTCTAACAGACAGACAGTAG---CACAGAAACTCCACGAAACCCAGAGCTGCCCTG 1438
Qy 3201 ATAGAACTCACTTTTCTACTGTTCTCTTAAGTGTGGAGTGAATGGAATTCCTCACTGTATGT 3260
Db 1439 TCAGAACT-ACTTCCATTAATCTCCCAATTTGGAGTAAGGGAATAATCCAGATGAATGC 1497
Qy 3261 TCACCTCTGAAGTGGGTACCCAGTCTCTTAATCTTTTGTATTTGCTCACAGTGTGGA 3320
Db 1498 TCGATCTGTGAGATGGGTGCCAGTCTCTGAAATCGTTTGTATTTTCTCACAGGCTCTGA 1557
Qy 3321 GCAGTCTGAGCAACAAAGCAGACACTCAATAAATGCT 3357
Db 1558 GCAATGTTGAACAAAGCCGAC-CTCAATAAATACT 1593

RESULT 4
Bi913504

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Bi913504 763 bp mRNA linear EST 16-OCT-2001
603179133F1 NIH_MGC_121 Homo sapiens cdna clone IMAGE:5243048 5',
mRNA sequence.
Bi913504
Bi913504.1 GI:16177911
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 763)
NIH-MGC <http://mgc.sci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM1613 row: b column: 09
High quality sequence stop: 675.

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FEATURES
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Location/Qualifiers
1. .763
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5243048"
/clone_lib="NIH_MGC_121"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dr primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MGC Library."
BASE COUNT 237 a 167 c 170 g 189 t
ORIGIN
Query Match 17.6%; Score 596.2; DB 10; Length 763;
Best Local Similarity 94.2%; Pred. No. 3.5e-113;
Matches 719; Conservative 0; Mismatches 28; Indels 16; Gaps 9;
QY 64 CTTGGCTCACAGGGGACGATGCAAGCTCTTCTGGCTCTCTTCTCAGCCTTGTCTGTGA 123
Db 1 CTTGGCTCACAGTGGAGCATGTCAAGCTCTTCTGGCTCTCTTCTCAGCCTTGTCTGTGA 60
QY 124 ACTGCTGCTCAGTCCACCAT-TGAGAACAGCCGACAGACATTTTGGACAAGTTTAAACA 182
Db 61 ACTGCTGCTCAGTCCACCATGTGAGAACAGCCGACAGACATTTTGGACAAGTTTAAACA 120
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QY 243 TACTGAAGAGAATGTCACAAACATGAATATCTGGGACAAATGGTCTGCTTTTAAA 302
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QY 303 GGAACAGTCCACACTTGCCCAATGTATCCACTACAAGAAATTCAGATCTCACAGTCAA 362
Db 241 GGAACAGTCCACACTTGCCCAATGTATCCACTACAAGAAATTCAGATCTCACAGTCAA 300
QY 363 GCTTCAAGTTCAGAGCTCTTTCAGCAAAATGGGTCCTCAGTGTCTCAGAGCAACAGCAA 422
Db 301 GCTTCAAGTTCAGAGCTCTTTCAGCAAAATGGGTCCTCAGTGTCTCAGAGCAACAGCAA 360
QY 423 ACGGTTGAACAAATTTCAATACAAATGAGCACCACATCTACAGTACTGGAAGAGTTGTAA 482
Db 361 ACGGTTGAACAAATTTCAATACAAATGAGCACCACATCTACAGTACTGGAAGAGTTGTAA 420
QY 483 CCAGATAATCCACAGAAATGCTTATTTACTTCAACAGGTTTGATGAATTAATGGCAAA 542
Db 421 CCAGATAATCCACAGAAATGCTTATTTACTTGAACAGGTTTGATGACATAATGGCAAA 480
QY 543 CAGTTTAGACTACAATGAGAGCTCTGGGCTTTGGGAAAGC---TGGAGATCTGAGTCTGG 599
Db 481 CAGTTTAGACTACAATGAGAGCTCTGGGCTTTGGGCAACCGCTGCGACATCTGAGTCTGG 540
QY 600 CAAGCAGCTGAGGCAATATATGAAGAGATGATGCTGTGTAATAA-ATGAGATGGCAAGAG 658
Db 541 CAAGCAGCTGAGGCAATATATGAAGAGATGATGCTGTGTAATAAATCAGATGGCAAGAG 600
QY 659 CAAATCATATGAGCACTATGGGATTTATGGAG-AGGAGACTATGAAGT--AAATGGGG 715
Db 601 CAAATCATATGAGCACTATGGGATTTATCGGAGAGAGAGACTATGAAGTACAAATGGGGT 660
QY 716 TAGATGGCTTATGACTACAGCCCGG-CCAGTTGATTGAA---GATGTGGAACATACCTTT 771
Db 661 AGCATGGCTATGACTACAGCCCGGAGCCAGCAAGTTCATTCGACGACTGTGGAACATACCTTT 720
QY 772 ----GAAGAGATTAAACCAATTATA-TGAACATCTTCATGCCTAT 810
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Db 721 TGACGAGACTTAACCCATTATACTGAACTCTTCATGCCTAT 763

RESULT 5
LOCUS BI561069 676 bp mRNA linear EST 05-SEP-2001
DEFINITION 603254275F1 NIH_MGC_97 Homo sapiens CDNA clone IMAGE:5296531 5',
mRNA sequence.

ACCESSION BI561069
VERSION BI561069.1 GI:15448383
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mhc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11750 row: f column: 20
High quality sequence stop: 674.
Location/Qualifiers
1. .676
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5296531"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"

note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
); Oligo-dr primed using primer 5'-TTTTTTTTTTTTTTN-3',
size-selected for average insert size 2.2 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 215 a 134 c 161 g 166 t
ORIGIN

Query Match 17.5%; Score 594.6; DB 10; Length 676;
Best Local Similarity 96.5%; Pred. No. 7.5e-113;
Matches 640; Conservative 0; Mismatches 19; Indels 4; Gaps 3;
QY 41 GAGCGCGCGCCGGGAGGATCTTGGCTCACAGGGACGATCTCAAGCTTCTCCTGGC 100
Db 14 GAAAGTCATTCACTGAGTGTATCTTGGCTCACAGGGAGCATGTCAGCTCTTCTGGC 73
QY 101 TCCCTTCTCAGCCTTGTGTGCTAACTGCTGCTCAGTCCACCATTTGAGAACAGGCCAAGA 160
Db 74 TCCCTTCTCAGCCTTGTGTGCTAACTGCTGCTCAGTCCACCATTTGAGAACAGGCCAAGA 133
QY 161 CATTTTGGACAAGTTTAAACCCAGCCGAGACCTGTCTTCTATCAAGTTCACCTGCT 220
Db 134 CATTTTGGACAAGTTTAAACCCAGCCGAGACCTGTCTTCTATCAAGTTCACCTGCT 193
QY 221 CTTGGAATTTAAACCAATATTACTGAAGAAATGTCCAAAACATGAATAATCTGCTGGG 280
Db 194 CTTGGAATTTAAACCAATATTACTGAAGAAATGTCCAAAACATGAATAATCTGCTGGG 253
QY 281 ACAATAGTCTGCTGCTTTTAAAGGAA-CAGTCCCACTTGCCCAATGTATCCACTACAA 339

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Db 254 ACAAATGGTCTGCCCTTTTAAAGGAAGCAGCTCCACACTTGGCCCAAAATGATATCCACTACAA 313
QY 340 GAAATTCAGAAATTCACAGTCAAGCTTCAGCTGCAGGCTCTTCAGCAAAAATGGGCTTTCA 399
Db 314 GAAATTCAGAAATTCACAGTCAAGCTTCAGCTGCAGGCTCTTCAGCAAAAATGGGCTTTCA 373
QY 400 GTGCTGTCAGAAAGCAAGCAAGCGTTGAACACATTTCTAAATACAATGAGCACCATC 459
Db 374 GTGCTGTCAGAAAGCAAGCAAGCGTTGAACACATTTCTAAATACAATGAGCACCATC 433
QY 460 TACAGTACTGAAAGTTTGTAAACCCAGATAATCCACAAGAAATGCTTATTTACTTTGAACCA 519
Db 434 TACAGTACTGAAAGTTTGTAAACCCAGATAATCCACAAGAAATGCTTATTTACTTTGAACCA 493
QY 520 GGTGTTGAATGAATTAATGGCAACAGTTTATAGCTACAAATGAGAGGCTCTGGGCTTGGGAA 579
Db 494 GGTGTTGAATGAATTAATGGCAACAGTTTATAGCTACAAATGAGAGGCTCTGGGCTTGGGAA 553
QY 580 AGCTGGAGATCTGAGTGGCAACAGCTGAGGCCATTTATGAAGAGTATGGGCTTTG 639
Db 554 AGCTGGAGATCTGAGTGGCAACAGCTGAGGCCATTTATGAAGAGTATGGGCTTTG 613
QY 640 -AAAAATGAGATGCAAGAGCAAAATCATATGAGG--ACTATGGGGGATTTATGGAGAGGA 696
Db 614 AAAAAATGAGATGCAAGAGCAAAATCATATGAGGACTATGGGGATTTATGGAGAGGA 673
QY 697 GAC 699
Db 674 GAC 676

RESULT 6
BG722079
LOCUS
DEFINITION BG722079 635 bp mRNA linear EST 08-MAY-2001
60269682F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4830668 5',
mRNA sequence.
ACCESSION BG722079
VERSION BG722079.1 GI:14001266
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 635)
NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10752 row: c column: 21
High quality sequence stop: 633.
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Location/Qualifiers
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1..635
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4830668"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (ctcgag
); Oligo-dr primed using primer 5'-TTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.2 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
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constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 202 a 131 c 144 g 158 t
ORIGIN
Query Match 17.1%; Score 581.8; DB 10; Length 635;
Best Local Similarity 98.4%; Pred. No. 3.4e-110;
Matches 619; Conservative 0; Mismatches 7; Indels 3; Gaps 3;
QY 51 CCGGGCAGGTATCTTGGCTCACA-GGGGACGATGTCAAGCTCTTCCTGGCTCTTCTCA 109
Db 9 CGGTGAGTGTATCTTGGCTCAGGGGACGATGTCAAGCTCTTCCTGGCTCTTCTCA 68
QY 110 GCCTTGTCTGTAACTGCTCTCAGTCCACCATTTGAGGAACAGGCAAGACATTTTGG 169
Db 69 GCCTTG-TGCTGTAACTGCTCTCAGTCCACCATTTGAGGAACAGGCAAGACA-TTTGG 126
QY 170 ACAAGTTTAAACACGAAGCGGAAGACCTTCTTATCAAAAGTTCACTTGCTTCTTGAAT 229
Db 127 ACAAGTTTAAACACGAAGCGGAAGACCTTCTTATCAAAAGTTCACTTGCTTCTTGAAT 186
QY 230 ATACACCAATATTTACTGAAGAGAAATGTCCAAAACATGAATATGCTGGGACAAATG 289
Db 187 ATACACCAATATTTACTGAAGAGAAATGTCCAAAACATGAATATGCTGGGACAAATG 246
QY 290 CTGCTTTTAAAGGAACAGTCCACACTTGCACCAATGTATCCACTACAGAAATTCACA 349
Db 247 CTGCTTTTAAAGGAACAGTCCACACTTGCACCAATGTATCCACTACAGAAATTCACA 306
QY 350 ATCTCAGTCAAGCTTTCAGCTGCAGGCTCTTCAGCAAAAATGGTCTTCAGTCTGTCTAG 409
Db 307 ATCTCAGTCAAGCTTTCAGCTGCAGGCTCTTCAGCAAAAATGGTCTTCAGTCTGTCTAG 366
QY 410 AGACAGAGCAAAACGGTGTGAACACAAATTTCTAAATCAATGAGCAGCACCCTACAGTACTG 469
Db 367 AGACAGAGCAAAACGGTGTGAACACAAATTTCTAAATCAATGAGCAGCACCCTACAGTACTG 426
QY 470 GAAAAGTTTGTAAACCCAGATAATCCACAGAAATGCTTATTACTTGAACAGGTTTGAATG 529
Db 427 GAAAAGTTTGTAAACCCAGATAATCCACAGAAATGCTTATTACTTGAACAGGTTTGAATG 486
QY 530 AAATAATGGCAAAACAGTTTGTAGACTACAAATGAGAGGCTCTGGGCTTGGGAAAGCTGGAGAT 589
Db 487 AAATAATGGCAAAACAGTTTGTAGACTACAAATGAGAGGCTCTGGGCTTGGGAAAGCTGGAGAT 546
QY 590 CTGAGTGTGCAAGCAGCTGAGGCCATTTATATGAAGAGTATGTGGTCTTGAATAATGAGA 649
Db 547 CTGAGTGTGCAAGCAGCTGAGGCCATTTATATGAAGAGTATGTGGTCTTGAATAATGAGA 606
QY 650 TGCAAGAGCAAAATCATTTATGAGGACTAT 678
Db 607 TGCAAGAGCAAAATCATTTATGAGGACTAT 635

RESULT 7
BG722079
LOCUS
DEFINITION BG722079 609 bp mRNA linear EST 05-SEP-2001
60325512F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5297380 5',
mRNA sequence.
ACCESSION BG722079
VERSION BG722079.1 GI:15448673
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 609)
NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
```

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11752 row: j column: 05
High quality sequence stop: 606.
Location/Qualifiers

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/clone="IMAGE:5297380"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dr primed using primer 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NHGRI/NIH). National Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT 193 a 128 c 137 g 151 t

Query Match 15.8%; Score 536.4; DB 10; Length 609;
Best Local Similarity 97.5%; Pred. No. 8.5e-101;
Matches 587; Conservative 0; Mismatches 11; Indels 4; Gaps 4;

QY 51 CGGGGCGAGTATCTTGGCTCACAGGGGACGATGTCAGCTCTTCTGCTCTCTCTCAG 110
| | | | |
Db 9 CAGTGGATGTGATCTTGGCTCACAGGGGACGATGTCAGCTCTTCTGCTCTCTCAG 68
QY 111 CTTTGTGCTGTAAGTCTGCTCAGTCCAGCAATGAGGACGACCAAGACATTTTGGGA 170
| | | | |
Db 69 COTATGTGCTGTAAGTCTGCTCAGTCCAGCAATGAGGACGACCAAGACATTTTGGGA 128
QY 171 CAAGTTTAAACGACGAGCGGACCTGTTCTATCAAGTTTCACTGCTCTCTTGAATTA 230
| | | | |
Db 129 CAAGTTTAAACGACGAGCGGACCTGTTCTATCAAGTTTCACTGCTCTCTTGAATTA 188
QY 231 TAACACCAATATTACTGAAGAGAAATGTCCAAACATGAATATGCTGGGGACAAATGTC 290
| | | | |
Db 189 TAACACCAATATTACTGAAGAGAAATGTCCAAACATGAATATGCTGGGGACAAATGTC 248
QY 291 TGCCTTTTAAAGGACAGTCCACACTTGGCCAAATGTATCCACTACAAGAAATTCAGA 349
| | | | |
Db 249 TGCCTTTTAAAGGACAGTCCACACTTGGCCAAATGTATCCACTACAAGAAATTCAGA 308
QY 350 ATCTCACAGTCAAGCTTCAGCTGCAGGCTCTTTCAGCAA-AATGGTCTTTCAGTGTGCA 408
| | | | |
Db 309 ATCTCACAGTCAAGCTTCAGCTGCAGGCTCTTTCAGCAAATGGTCTTTCAGTGTGCTCA 368
QY 409 GAAGACAGAGCAACGGTGTGAACAC-AATTCTAAATACAATGAGCACCATCTACAGTAC 467
| | | | |
Db 369 GAAGACAGAGCAACGGTGTGAACACGAATCTAAATACAATGAGCACCATCTACAGTAC 428
QY 468 TGGAAAGTTGTACCCAGATATCCACAGAAATGCTTTATTTACTTGAACCCAGGTTGAA 527
| | | | |
Db 429 TGGAAAGTTGTACCCAGATATCCACAGAAATGCTTTATTTACTTGAACCCAGGTTGAA 488
QY 528 TGAATAATGCAACAGCTTTAGACTACAATGAGAGGCTCTGGGCTTGGGAAGCTGGAG 587
| | | | |
Db 489 TGAATAATGCAACAGCTTTAGACTACAATGAGAGGCTCTGGGCTTGGGAAGCTGGAG 548
QY 588 ATCTGAGTCCGCAAGCTGAGGCCATTATATGAAGAGTATGTGGTCTTTGAATAATGA 647
| | | | |
Db 549 ATCTGAGTCCG-AAGCAGCTGAGGCCATTATATGAAGAGTATGTGGTCTTTGAATAATGA 607
QY 648 GA 649

Db 608 CA 609

||

RESULT 8

BC962298

LOCUS

DEFINITION

BC962298

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

602827090F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4981606 5',

mRNA sequence.

766 bp mrna linear EST 12-JUN-2001

GI:14349935

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 766)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-femail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM10983 row: d column: 23

High quality sequence stop: 708.

Location/Qualifiers

1..766

/organism="Mus musculus"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:4981606"

/clone_lib="NCI_CGAP_Co24"

/lab_host="DH10B (T1 phage-resistant)"

/note="Organ: colon; Vector: PCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.

Average insert size 1.6 kb. Constructed by Life

Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 233 a 156 c 179 g 198 t

ORIGIN

Query Match 14.8%; Score 502.8; DB 10; Length 766;

Best Local Similarity 85.3%; Pred. No. 7.7e-94;

Matches 631; Conservative 0; Mismatches 102; Indels 7; Gaps 6;

QY 1327 AAGCATTTAAATCCATTGGTCTTCTGTCACCCGATTTTCAAGAGACAAATGAACAGAA 1386

| | | | |

Db 2 AAGCATCTGAATCCATTGGTCTTCTGCCATCCGATTTTCAAGAGATAGCGAAACAGAG 61

| | | | |

QY 1387 ATAACTTCCTGCTCAAAACAGCACTCACGATTTGGGACTCTGCCATTTACTTACATG 1446

| | | | |

Db 62 ATAACTTCCTGCTCAAAACAGCACTCACGATTTGGGACTCTGCCATTTACTTACATG 121

| | | | |

QY 1447 TTAGAGAGTGGAGTGGATGGTCTTTAAAGGGGAAATCCCAAGACCAAGTGGATGAA 1506

| | | | |

Db 122 TTAGAGAGTGGAGTGGATGGTCTTTCCGGGTGAAATCCCAAGACCAAGTGGATGAA 181

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QY 1507 AAGTGGTGGGAGATGAAGCGAGAGATAGTTGGGTGCTGGAACCTGCCCCCATGATGAA 1566

| | | | |

Db 182 AAGTGGTGGGAGATGAAGCGGAGATCGTTGGTGGTGGGCTCTGCCCTCATGATGAA 241

| | | | |

QY 1567 ACATCTGTGACCCCGCATCTCTGTTCCATGTTTCTAATGATTACTCATTTCCGATAT 1626

| | | | |

Db 242 ACATCTGTGACCCCGCATCTCTGTTCCATGTTTCTAATGATTACTCATTTCCGATAT 301

| | | | |

QY 1627 TACACAGGACCCCTTACCAATTTCCAGTTTCAAGAGACACTTTGTCAAGCAGGTAACAT 1686

| | | | |

Db 302 TACACAGGACCCCTTACCAATTTCCAGTTTCAAGAGACACTTTGTCAAGCAGGTAACAT 361

| | | | |

QY 122 TAAGTGTGCTGCTAGTCCACCATGTTAGGACAGGCGCAAGACATATTTTGGACAAGTTTAACC 181
 Db 60 TTACTACTGCTAGTCCCTCAGGAGGAATGCCAAGACATATTTTAAACAACCTTAATC 119
 QY 182 ACGAAGCCGAGACCTGTTCTATCAAGTTCACCTTCTTGTGAATATTAACACCAATA 241
 Db 120 AGGAAGCTGAAGACCTGTTCTTAAAGTTCACCTTCTTGTGAATATTAACACCAATA 179
 QY 242 TTACTGAAGAAGATGTCACCAACATGAATGCTGGGACAAATGGTCTGCCTTTTAA 301
 Db 180 TTACTGAAGAAGATGTCACCAACATGAATGCTGGGACAAATGGTCTGCCTTTTAA 239
 QY 302 AGGACAGTCCACACTTCCCAAAATGATCCTACCTACAGAAATTCAGAACTCACAGTCA 361
 Db 240 AAGAACAGTCTAAGACTGCCAAAGTCTCTACTACAGAAATTCAGAACTCCAGTCAATCA 299
 QY 362 AGCTTCAGTGCAGGCTTTCAGCAAAATGGGTCTTTCAGTCTCTCAGAGCAAGAGCA 421
 Db 300 AGCTCAACTACAGGCGCTTTCAGCAAAATGGGTCTTTCAGTCTCTCAGAGCAAGAGCA 359
 QY 422 AACGGTTGAACAAATCTTAATACATGAGCACCCTACAGTCTGGAAGCTGGAAGTTGTA 481
 Db 360 AACAGTTGAACAAATCTTAATACATGAGCACCCTACAGTCTGGAAGCTGGAAGTTGTA 419
 QY 482 ACCAGATAATCCACAGAAATGCTTATTACTTGAACACAGGTTTGAATGAATAATGSCAA 541
 Db 420 ACCAAAGAACCCACAGAAATGCTTATTACTTGAACACAGGATTGGATGAATAATGSCGA 479
 QY 542 ACAGTTTAGACTACATGAGAGGCTCTGGCTTGGGAAGCTGAGATCTGAGGTGCGCA 601
 Db 480 CAGACAGACTACAACTCTAGGCTCTGGGCATGGGAGGCTGGAGGCTGAGGTGGCA 539
 QY 602 AGCAGCTGAGGCGCATATATGAGAGATGATGGTCTTGAAGAAATGAGATGSC-AAGAGCA 660
 Db 540 AGCAGCTGAGGCGCATATGAGAGATGATGGTCTTGAAGAAATGAGATGSCAAAGAGCA 599
 QY 661 AATCATATGAGCACTGGGATATGAGAGAGGACTATGAATGAATGGGTGAT 720
 Db 600 AACATATTAACCACTATGGGATATGAGAGGAGGACTATGAAGCAGAGGAGCAGAT 659
 QY 721 GGCTATGACTACAGCGCGCCAGTGTGATGAAGATGTGGAACATACCTTTGAAGAGATT 780
 Db 660 GGTAACTATAACCGGTAAACAGTATGAGATGTGAACGTACTTGGC-----AGAAA 712
 QY 781 AAACCATATTAACCACTATGCTGCTATGCTATGAGAGGCA 819
 Db 713 TCACATGGGTGAGCTCTTATGCTATGAGGGGA 751

RESULT 12
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 LOCUS hn74h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3033655 3',
 DEFINITION mRNA sequence.
 ACCESSION AW772472
 VERSION AW772472.1 GI:7704538
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 462)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Christopher Moshaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
 Seq primer: -400P from Gibco
 High quality sequence stop: 453.
 Location/Qualifiers
 1. 462
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3033655"
 /clone_lib="NCI_CGAP_Kid11"
 /lab_host="DH10B"
 /note="organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following NIP hybridization, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo."
 BASE COUNT 132 a 98 c 100 g 132 t
 ORIGIN

Query Match 13.5%; Score 458.8; DB 9; Length 462;
 Best Local Similarity 99.6%; Pred. No. 1e-84;
 Matches 460; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2908 ACTGGGTACTGCAGGATTGAGAAATGCGATGCAATAGCTCACTTTCATTTAATCCATT 2967
 Db 462 ACTGGTGTCTGCTCAAGGATTGAGAAATGCGATGCAATAGCTCACTTTCATTTAATCCATT 403
 QY 2968 GTCAAGGATGACATGCTTCTTTCACAGTAACCTCAAGTACTATGCTGATTTGCTA 3027
 Db 402 GTCAAGGATGACATGCTTCTTTCACAGTAACCTCAAGTACTATGCTGATTTGCTA 343
 QY 3028 CAGTGATGTTGAATCGATCATGCTTCTTCAAGTGACAGGCTTAAGAGAGAGAAAT 3087
 Db 342 CAGTGATGTTGAAATCGATCATGCTTCTTCAAGTGACAGGCTTAAGAGAGAGAAAT 283
 QY 3088 CCAGGGAACAGGTAGAGGACATTTCTTTTCACTTTTCAAGGTGCTTGATCAACATCTCCC 3147
 Db 282 CCAGGGAACAGGTAGAGGACATTTCTTTTCACTTTTCAAGGTGCTTGATCAACATCTCCC 223
 QY 3148 TGACACACAAAACCTAGAGCCAGGCGCTCCGTAACCTCCAGAGCATGCCGTGATAGAA 3207
 Db 222 TGACACACAAAACCTAGAGCCAGGCGCTCCGTAACCTCCAGAGCATGCCGTGATAGAA 163
 QY 3208 CTCATTTCTACTGTTCTTAACCTGTGAGTGAATGGAATTCACAACTGATGTTTCAACCT 3267
 Db 162 CTCATTTCTACTGTTCTTAACCTGTGAGTGAATGGAATTCACAACTGATGTTTCAACCT 103
 QY 3268 CTGAAGTGGGTACCCAGTCTCTTAATCTTTTGTATTTGCTCACAGTGTGACAGTGC 3327
 Db 102 CTGAAGTGGGTACCCAGTCTCTTAATCTTTTGTATTTGCTCACAGTGTGACAGTGC 43
 QY 3328 TGAGCACAAGAGCAGACACCAATTAATGCTAGATTATACACAC 3369
 Db 42 TGAGCACAAGAGCAGACACCAATTAATGCTAGATTATACACAC 1

RESULT 13
 BB652968
 LOCUS BB652968
 DEFINITION BB652968 RIKEN full-length enriched, adult male hippocampus Mus musculus cDNA clone C630041D11 5', mRNA sequence.
 ACCESSION BB652968
 VERSION BB652968.1 GI:15402926
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;


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http://image.llnl.gov
Plate: LLCMI367 row: n column: 18
High quality sequence stop: 450.
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        /clone_lib="NIH_MGC_75"
        /lab_host="DH10B (T1 phage-resistant)"
        /note="Organ: Kidney; Vector: pDNR-LIB (Clontech); Site 1:
        SfiI (ggccctcgcc); Site 2: SfiI (ggccattggcc); 5' and
        3' adaptors were used in cloning as follows: 5' adaptor
        sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:
        5'-ATCTAGAGCCGAGCGCGGCACATG-dT(30)BN-3' (where B = A,
        C, or G and N = A, C, G, or T). Average insert size 1.65
        kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
        by PCR. This library was enriched for full-length clones
        and was constructed by Clontech Laboratories (Palo Alto,
        CA). Note: this is a NIH_MGC Library."
BASE COUNT      144 a      81 c      103 g      124 t
ORIGIN
    Query Match      13.3%; Score 451; DB 10; Length 452;
    Best Local Similarity 100.0%; Pred. No. 4.1e-83;
    Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1788 ATTGGAAATGTTGTAGGAGCAAGAACATGAATGTAAAGGCACCTGCTCAACTACTTTGA 1847
Db 1 ATTGGAAATGTTGTAGGAGCAAGAACATGAATGTAAAGGCACCTGCTCAACTACTTTGA 60
QY 1848 GCCCTTATTACCTGGCTGAAGACCAAGCAAGAAATCTTTTGTGGATGGATACCGA 1907
Db 61 GCCCTTATTACCTGGCTGAAGACCAAGCAAGAAATCTTTTGTGGATGGATACCGA 120
QY 1908 CTGAGTCCATATGCAGACCAAGCATCAAGTGAAGTGAAGTAAAGTCAAGTCAAGTCTTGG 1967
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VERSION        AI628611.1 GI:4665411
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SOURCE         human.
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               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      *1 (bases 1 to 447)
```

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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POLYA-No.

Location/Qualifiers
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a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(clones 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo."

BASE COUNT 127 a 89 c 97 g 134 t
ORIGIN

Query Match 13.0%; Score 440.6; DB 9; Length 447;
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Matches 443; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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